

Fig. 2 A



Fig. 2B

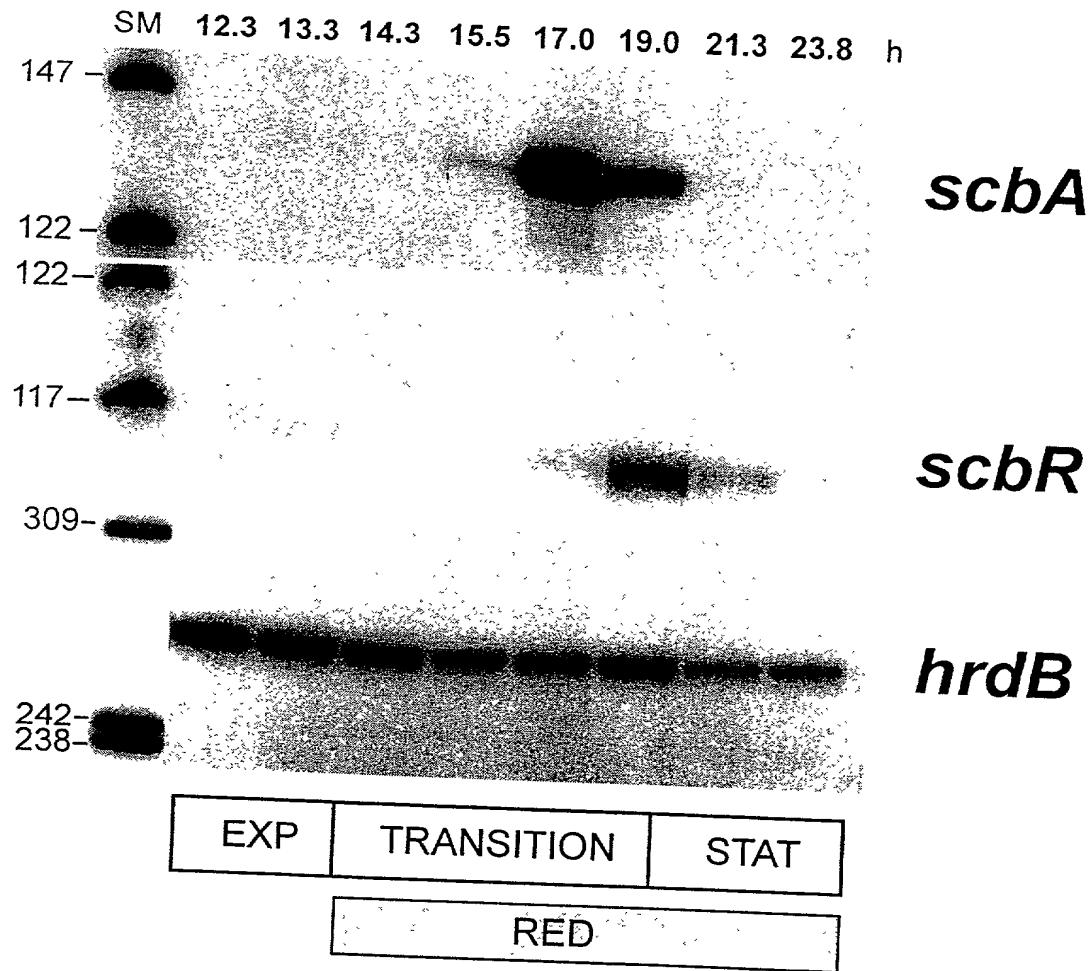


Fig. 3A

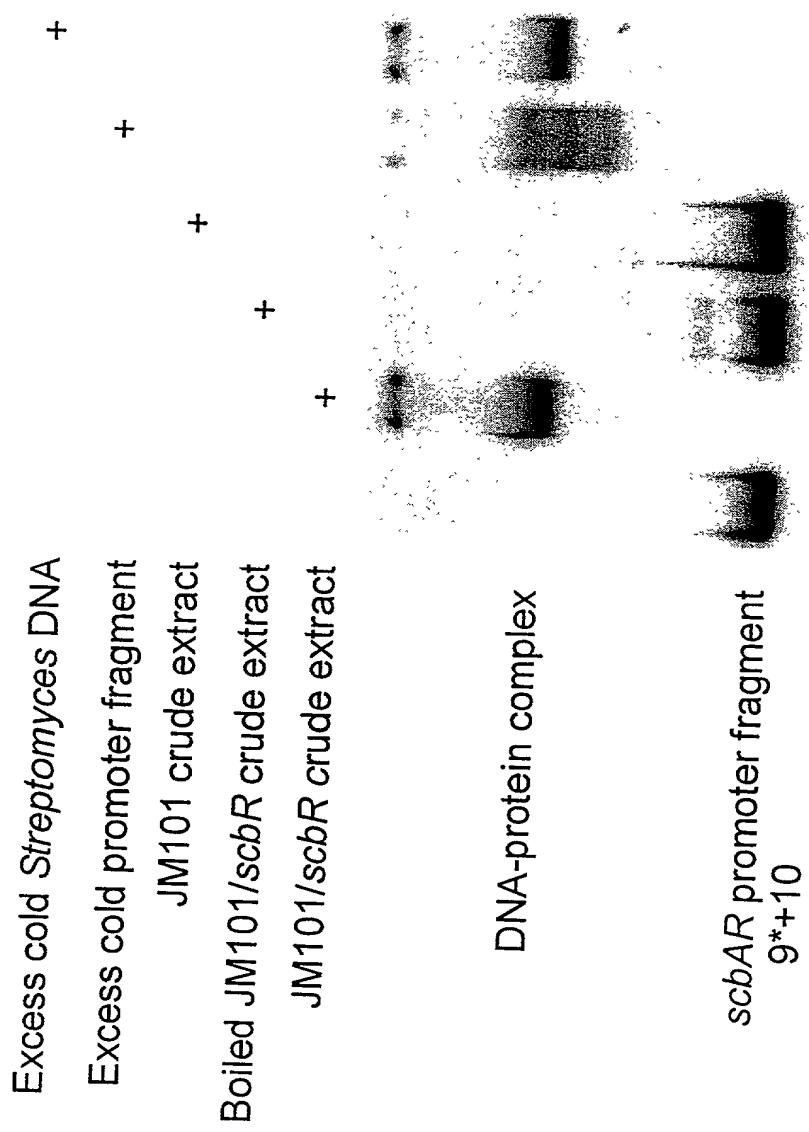


Fig. 3B

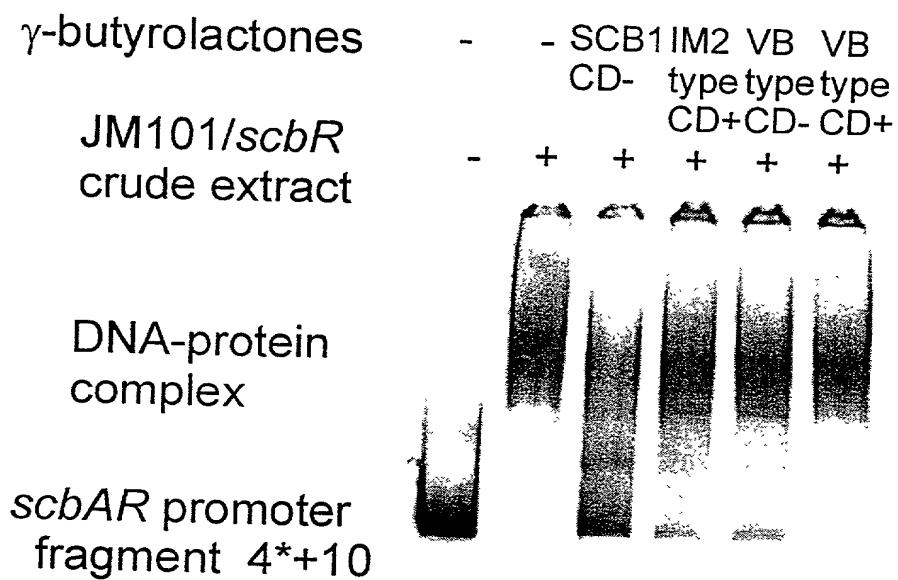


Fig. 4 A

## PCR fragment

\*labelled oligo

$$9^*+10$$

JM101/*scbR*  
crude extract

— +

9+10\*

\_\_\_\_\_

protein

concentration ( $\mu$ l)

A G

G A

2.5 1.25 0.16

1 | No. 1

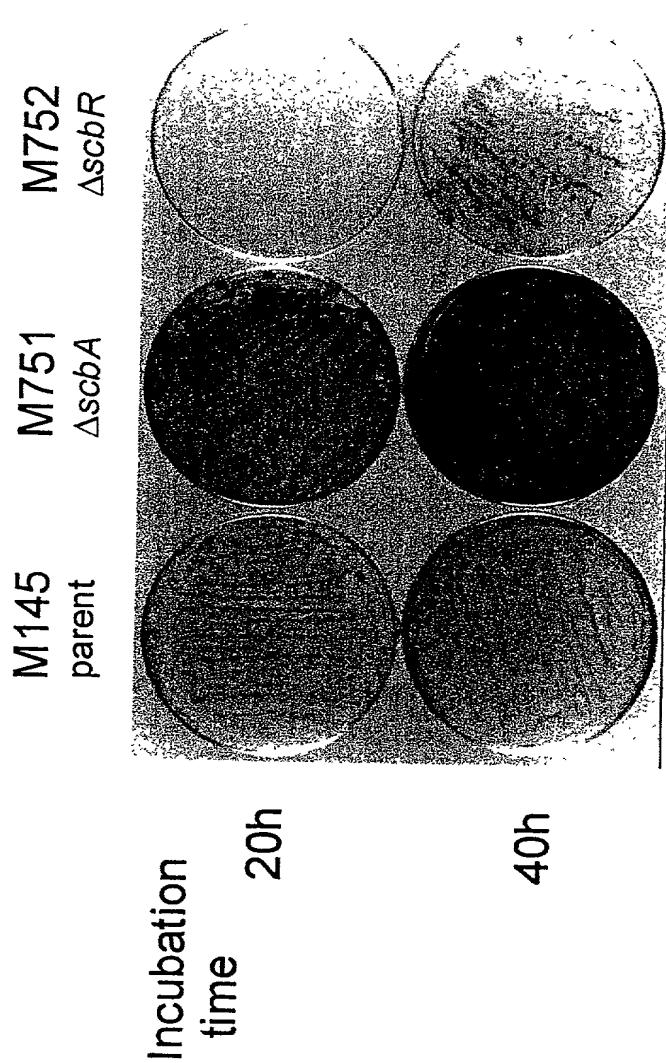
| No.2

No.2

fig. 48

GGGCAGGACGGCGGTGACCGAGAACCGGTACCGCCCTCGGTATCCAGCTGACCAGGGAA  
 1 -----+-----+-----+-----+-----+-----+-----+ 60  
 CCCGTCCCTGCCGCCACTGGCTCTTGGCCAGTGGCGGGAAAGCCATAGGTGACTGGCCCTT  
 P L V A T V S F R D G G K P I W S V P F  
 -67 binding site No.2  
 CGCGTCCTGCACCCCTGGTCCGGTGGACAAGGCCATCGAACCGGCAATGCGGTTGTT  
 61 -----+-----+-----+-----+-----+-----+-----+ 120  
 GCGCAGGACGTGGGACCAGGCCACCTGTTCGCGGTAGCCTGGCCGTTACGCCAAACAAG  
 A D Q V R T R H V L A M P V P L A T Q E  
 -41 +1 pscbR  
 GATCGAGTTGGCATCGGACGCAGAATTGATCAAAACTACTGCTTCGGCATGGTCCCCC  
 121 -----+-----+-----+-----+-----+-----+-----+ 180  
 CTAGCTCAACCGTAGCCTGCGTCTTAACTAGTTGATGACGAAGCCGTACCCAGGGGG  
 I S N A D S A S N I L V V A E P M [ScbA]  
 CCAGGAATCATGTGATGCCGAGCTGTTCTGTATGCGCGAACGTTAAGATAACAGACTGAGC  
 181 -----+-----+-----+-----+-----+-----+-----+ 240  
 GGTCTTAGTACACTACGGCTCGACAAGACATACGCGCTTGCAATTCTATGTCTGACTCG  
 pscbA ← +1 -4 binding site No.1  
 GGTTTTTTCTATCCTCCGGGGAGACATGAACAAGGAGGCAGGCATGGCAAGCAG  
 241 -----+-----+-----+-----+-----+-----+-----+ 300  
 CCAAAAAAAAGATAGGAAGGGCCCCCTGTACTTGTCTCCGTACCGGTTCGTC  
 -33 [ScbR] M A K Q  
 GACCGGGCGATCCGCACGCCAGACGATCCTGGACGCCGCGCAGGTCTCGAGAAG  
 301 -----+-----+-----+-----+-----+-----+-----+ 360  
 CTGGCCCGCTAGGCGTGCGCCGTCTGCTAGGACCTGCCGCCGTCCAGAAGCTCTTC  
 D R A I R T R Q T I L D A A A Q V F E K  
 CAGGGCTACCAAGCTGCCACGATCACGGAGATCCTCAAGGT  
 361 -----+-----+-----+-----+-----+ 401  
 GTCCCGATGGTTCGACGGTGCTAGTGCCTCTAGGAGTTCCA  
 Q G Y Q A A T I T E I L K

Fig. 5 A



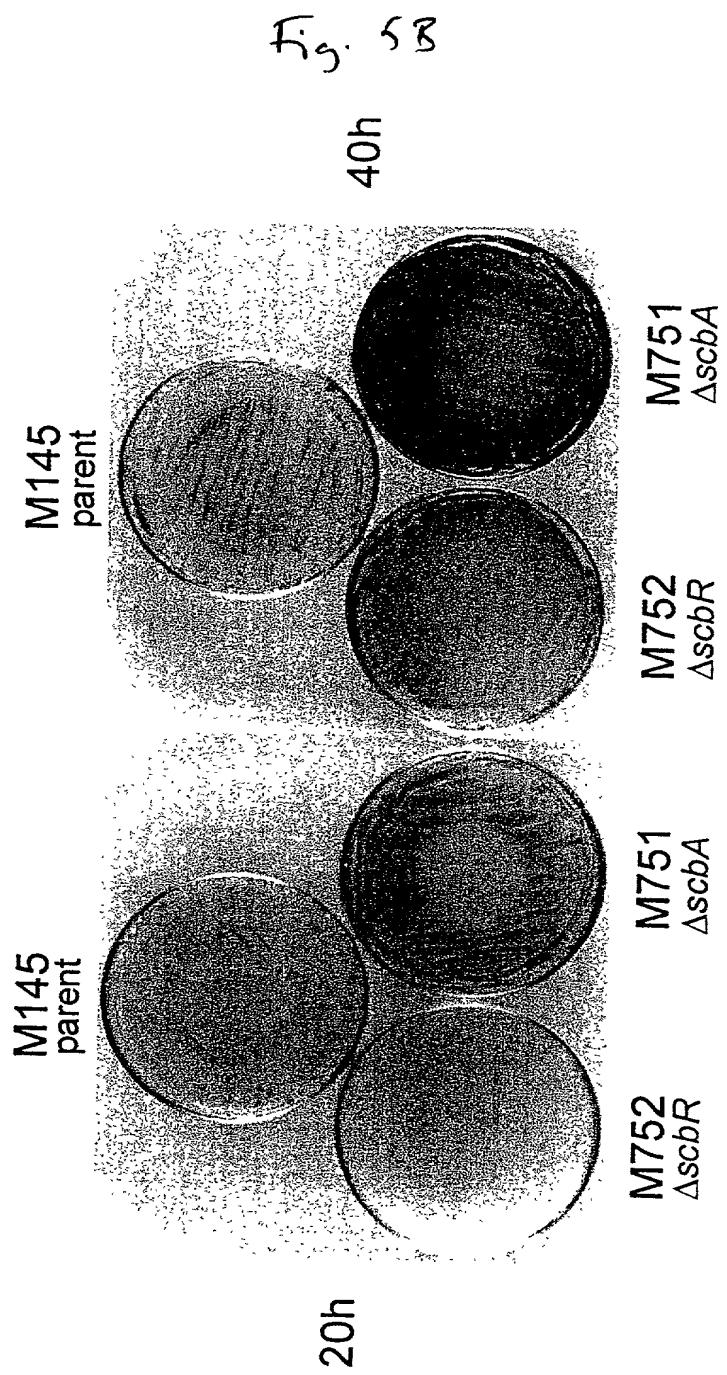
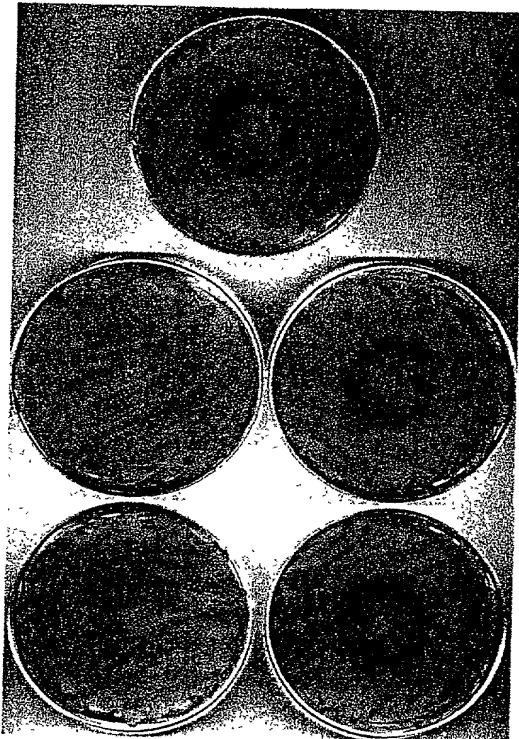


Fig. 6

M145(*pset152*)



M751(*pset152*)

M751(*scbA*)

M752(*pset152*)

M752(*scbR*)

M145                    M751                    M752

1 2 3 4 5 6 1 2 3 4 5 6 1 2 3 4 5 6

*scbA*



*scbR*



*hrdB*



E	TRAN	S	E	TRAN	S	E	TRAN	S
RED				RED			RED	
								A

Act production (ng/ml)	1) 12.0 2) 52 3) 6) 200	1) 6.0 3) 250 6) 1844	1) 2.0 3) 6.0 6) 288
Red production (μg/ml)	1) 0.26 3) 0.44 6) 0.67	1) 0.06 3) 2.08 6) 6.40	1) 0 3) 0 6) 0.15

Fig. 7B

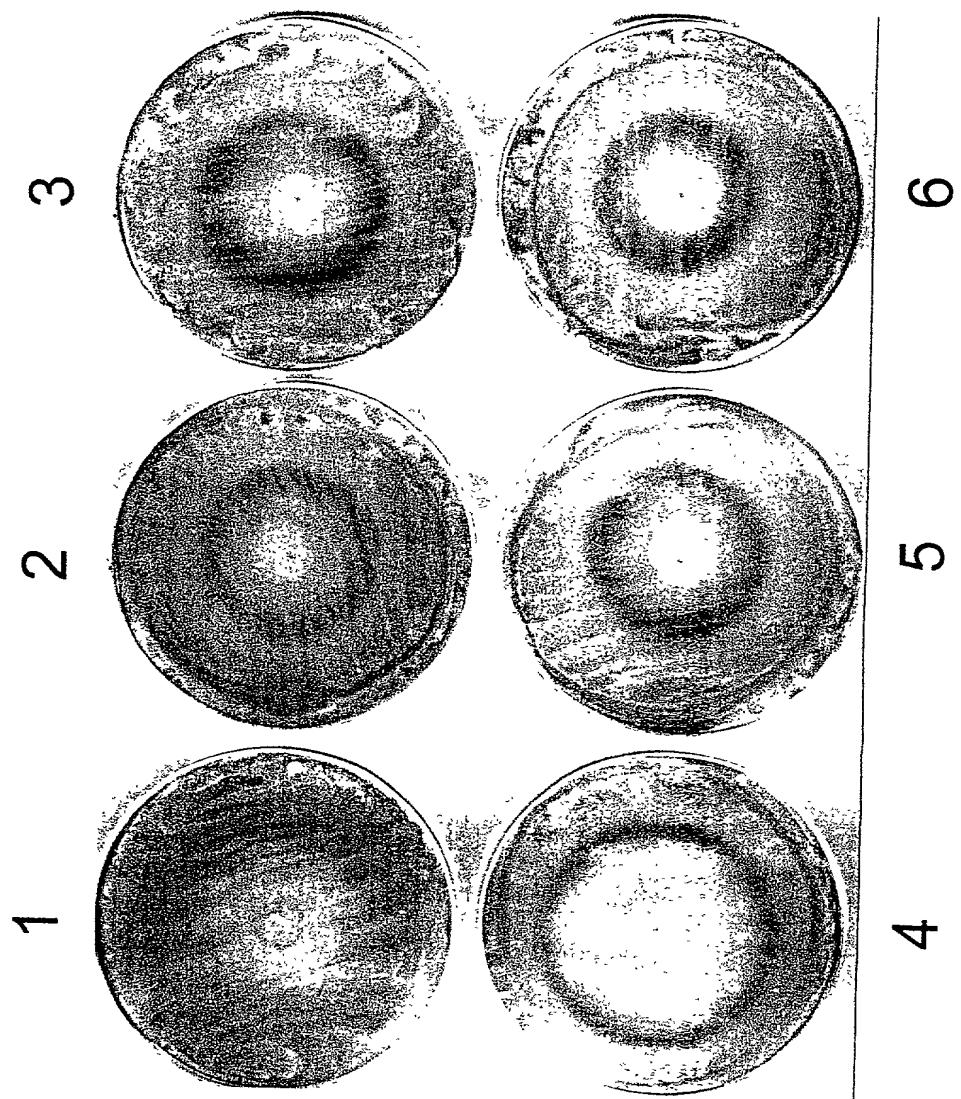


Fig. 8

SCB1  
concentration

0 ng  
31.25 ng

*scbA*

*scbR*

*hrdB*

Fig. 9: ScbR amino acid sequence

MAKQDRAIRTRQTILDAAAQVFEKQGYQAATITEILKVAGVTKG  
ALYFHFQSKEELALGVFDAQEPPQAVPEQPLRLQELIDMGMLFCHRLRTNVVARAGVR  
LSMDQQAHGLDRRGPFRRWHETLLKLLNQAKENGELLPHVVTDSADLYVGTFAGIQV  
VSQTVSDYQDLEHRYALLQKHILPAIAVPSVLAALDLSEERGARLAAELAPTGKD

Fig. 10: ScbA amino acid sequence

MPEAVVLINSASDANSIEQTALPVPMALVHRTRVQDAFPVSWIP  
KGDRFSVTAVLPHDHPFFAPVHGDRHDPLLIAETLRQAAMLVFHAGYGVPGYHFLM  
TLDYTCHLDHLGVSGEVAELEVEVACSQLKFRGGQPVQGQVDWAVRRAGRLAATGTA  
TTRFTSPQVYRRMRGDFATPTASVPGTAPVPAARAGRTRDEDVVLASSQQDTWRLRV  
DTSHPTLFQRPNHDVPGMLLEAARQAACLVTGPAPFVPSIGGTRFVRYAEFDSPCWI  
QATVRPGPAAGLTTVRTGHQDGSLVFLTTLSGPAFSG

Fig. 11: ScbB amino acid sequence

MRAHGTRYGRPLEGKTALVTGGSRGIGRGIALRLAADGALVAVH  
YGSSEAAARETVETIRSSGGQALAIRAELGVVGDAALYAAFDAGMGEFGVPPEFDIL  
VNNAGVSGSGRITERVTEEVFDRLVAVNVRAPLFLVQHGLKRLRDGGRIINISSAATRR  
AFPESIGYAMTKAVDTLTLALARQLGERGITVNAVAPGFVETDMNARRQTPEAAAA  
LAAYSVFNRIGRPPDIADVVAFLASDDSRWITGQYVDAATGGTIL

Fig. 12

## Act Production by *S. lividans* Strains Carrying pIJ68

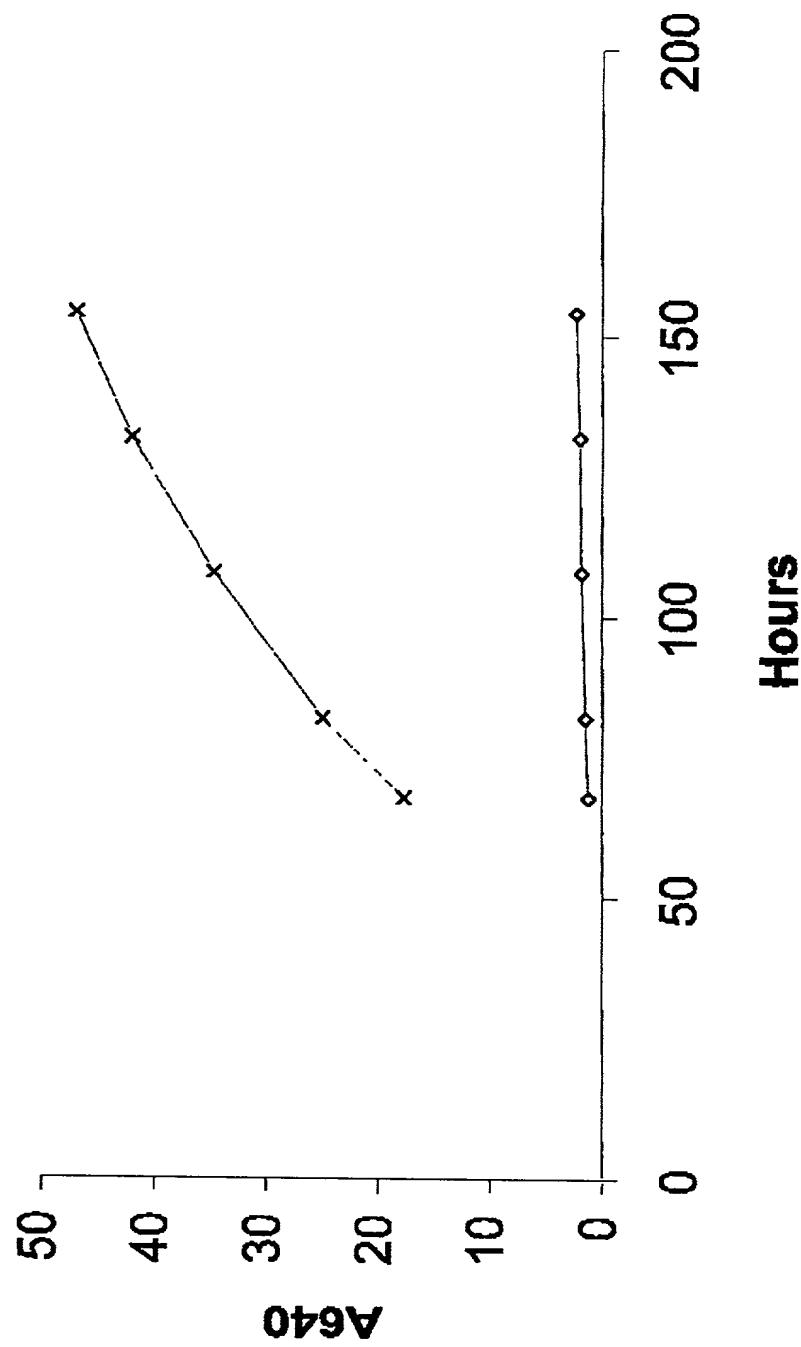


Fig. 13

## Red Production by *S. lividans* Strains Carrying plJ6014

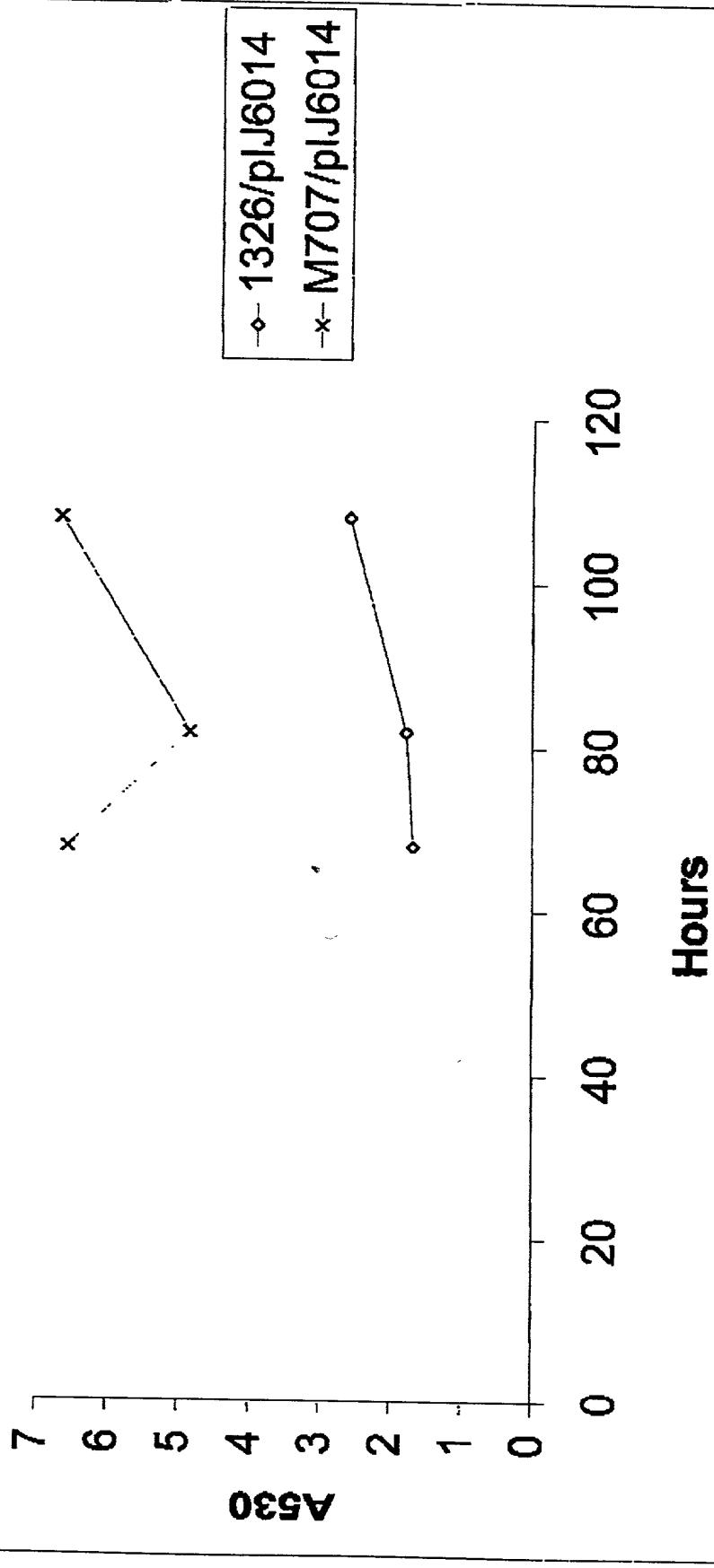


Fig. 14

DNA\_SEQUENCE Length: 4346kb..

1 **GTCGAC**GACG GCGTCGGGTT CGACGCCGAC GCGGTACTCG TTCCCGGCCA  
*HincII*

51 CCGGGCACCG GGTCTGCGCT CGATGACCGA CCGCATCGAG GACGTCGGCT

101 GGCGGCTCCT GATA GTGAGC GGCCCCGCCG GCGGCACGCA CATCGACGTC

151 CATCTCCCAC TGCGCCCCCG GAAAGTGAGC ACCGCACCGC GGACGTGACG

201 CCATGGGAGG GCCACGTCCG CGGACGGATC ACCCCTGGCT TCGGCCGAAG

251 GCTTCCGCGT GGTCCGCCGC CCAGATGCGG AACGGCCTGG CGGGCCGGCC

301 CGTCACTTCC CGCACGGTCG GCACGACCTG CGCCTTGGCC CCCGCCCGCT

351 GCCGCTCGGC GCTCTCCAGG AACGCGTCGG CGACGGGCCT CGGATACTTC

401 CGGAGCATCT GCTCGCGCGC CGCCTCCAGC CCCAGCTCCT CGAAACGCAG

451 TGACCGCCCC AGCACCTCGG AGAGCCGCGC CGTCTGCTGC CTGGCGGTGA

501 TCGCCTCGGG CCCGGACAGC GCGTACGCCCG GTCCCTCGTG GCCGGGCCGG

551 GTCAGTGCAC TGACCGCCAC TTCCCGGATG TCGCGCGGAT CGACGCAGGC

601 AACCGGGGAC GTGCCGTACA GCGCGCGGAC CACGCCGTG GACCGGATGG

651 CGGGCGCCCA GGACAGCGTG TTGGACATGA AGGTCTGGC CCGCAGGAAG

701 GTCCAGTCTA GCCCGGACTC GCGTACGCCCG CGCTCGTTCT CGCGCTGCCG

751 CCGCGTGATG AAGTCGTCCG CGCCCGGTTG CCCCACCGCG AGCATGGACA

801 GCTTCACCAG GTGCCGGACG CCGGCCTCGC GCGCCGCCGC CGCGAAACGC

851 TCGTCGTCCG GCTCGGTGGC ACTGTTCTG ACGAGGAACG CCGCCCGCAC

901 CCCGTTGAGG GCCCGGTCCA GGCCCGGGCG GTCGCGTAC TCGCCCGCGC

951 AGACCTCGAC GTTCGGGCCG GTGACGGTCA CCCGTTCCGG CCGCCGGCG

1001 AGGACTCTGA CGGGACCGGT CGGGGCCAGC AGGTGGGCGA CCTGACGGCC

1051 GACCACACCG GTCACGCCGG TCACAAAGAAT CACTCGGGGC TCCTCTCGGG

1101 CAGCGAGGCA GGGCGCCTC CGAACATACA TATGAGGGGA Agggcaggat

1151 ctgccccggg gcgcgaaaccg gcgatgttcg cgccccGGGG CCGGTGCTTC

1201 AGCCGGAGAA CGCGGGGCCG GACAGCGTGG TGAGGAAGAC GAGGCTGCCG

1251 TCCTGATGCC CGGTGACCCG CACGGTGGTC AGCCCCGCCG CGGGCCCCGG

1301 CCGGACCGTC GCCT**GGATC/C** AGCACGGCT GTCGAACTCC GCGTACCGGA

*BamHI*

1351 CGAACCGGGT GCCGCCGATC GACGGCACGA AGGGCGCCGG ACCGGTCACG  
 1401 AGGCACGCCG CCTGCCGTGC CGCCTCGAGC AGCAGCATGC CCGGTACGTG  
 1451 GTCGTTGGGG CGCTGGAAGA GGGTCGGGTG ACTGGTGTCC ACCCGCAGTC  
 1501 GCCACGTGTC CTGCTGCGAA CTCGCCGACA GGACCACGTC CTCGTCGCGG  
 1551 GTGCGACCAGG CGCGCGCCGC GGGCACGGGC GCGGTCCCGG GCACCGATGC  
 1601 GGTGGGAGTC GCGAAGTCGC CGCGCATCCG CCGGTAGACT TGAGGACTGG  
 1651 TGAAGCGCGT CGTGGCAGTC CCCGTGGCAG CGAGCCGTCC GGCGCGGC  
 1701 ACGGCCAGT CCACCTGTCC CTGTACGGGC TGCCCGCCGC GGAACTTCA  
 1751 CTGGGAACAG GCCACTTCCA CCTCCAGCTC CGCGACCTCG CCCGACACGC  
 1801 CGAGGTGGTC GAGGTGGCAG GTGTAGTCCA GCGTGGCCAT CAGGAAGTGG  
 1851 TAGCCCACCG GCACGCCGTA GCCGGCGTGG AAGACGAGCA TCGCCGCCTG  
 1901 ACGCAGGGTC TCGCGATCA GCAGCGGATC GTGTCGGTCC CCGTGGACCG  
 1951 GTGCGAAGAA CGGGTGGTCG TGGGGCAGGA CGGCGGTGAC CGAGAACCGG  
 2001 TCACCGCCCT TCGGTATC**CA** **G/CTGACCGGG** AACGCGTCCT GCACCCTGGT

*Pvu*II

2051 CCGGTGGACA AGCGCCATCG GAACCGGCAA TCGGGTTTGT TCGATCGAGT  
 2101 TGGCATCGGA CGCAGAAATTG ATCAAAACTA CTGCTTCGGG CATGGGTCCC  
 2151 CCCCAGGAAT CATGTGATGC CGAGCTGTT TGTATGCGCG AACGTTAAGA  
 2201 TACAGACTGA GCGGTTTTTT TTCTATCCTT CCCGGGGGAG ACATGAACAA  
 2251 GGAGGCAGGC ATGGCCAAGC AGGACCGGGC GATCCGCACG CGGCAGACGA  
 2301 TCCTGGACGC CGCGCGCGAG GTCTCGAGA AGCAGGGCTA CCAAGCTGCC  
 2351 ACGATCACG/G AGATCCTCAA GGTGGCCGGG GTGACCAAGG GAGCCCTCTA

**CTGCA/GATG** designed primer to generate *Pst*I site

*Pst*I

2401 CTTCCACTTC CAGTCCAAGG AAGAACTGGC GCTGGCGTC TTCGACGCC  
 2451 AGGAACCACC ACAGGCCGTT CCGGAGCAAC CCCTCCGGCT GCAAGAACTC  
 2501 ATCGACATGG GCATGTTGTT CTGTCACCGC TTGCGCACGA ACGTCGTGGC  
 2551 CCGGGCCGGC GTGCGCCTCT CCATGGACCA GCAGGCGCAC GGTCTCGATC  
 2601 GCCGAGGACC CTTCCGTCGC TGGCACGAGA CACTCCTGAA GCTGCTGAAC  
 2651 CAGGCCAAGG AGAACGGTGA GTTGCTGCC CATGTGGTCA CCACCGACTC  
 2701 GGCCGATCTC TACGTGGCA CGTTCGCCGG GATAACAGGTC GTGTCCCAGA  
 2751 CGGTCAAGCGA CTACCAGGAC CTCGAACACC GCTACCGCGCT **GCTGCA/GAAG**

*Pst*I

2801 CACATCCTGC CGGCCATCGC GGTTCCCTCC GTGCTGGCCG CGCTCGATCT  
 2851 CTCCGAGGAG CGCGGAGCAC GCCTCGCGC CGAACTGGCA CCGACCGGGA  
 2901 AGGACTGACC GCCGAAGCGC CCGCACCGGA TACCGACCCG CCGTGCCCCGA  
 2951 GCGGCCGACC GGGGCCGCCT ACGGGCCCGG CGGCAGGGCCC GTAGGTCTGC  
 3001 CCTGCGTACC GAAGCGTGGC GGGTCAGAGA ATCGTTCCGC CTGTGGCATC  
 3051 GACGTACTGG CCGGTGATCC ACCGTGAGTC GTCGGAGGCC AGAAAGGCCA  
 3101 CCACGTCGGC GATGTCGTCG GGTCTGCCGA TGCGGTTGAA CACGGAGTTG  
 3151 GCGGCCAGTG CCGCGGCCGC CTCGGGGTC TGCCGCCGCC GTGCGTTCAT  
 3201 GTCCGTCTCC ACGAAACCCG GCGCCACCGC GTTGACCGTG ATCCCCCGTT  
 3251 CCCCCAGTTG CCTGGCCAGG GCGAGCGTGA GCGTGTCCAC CGCACCCCTG  
 3301 GTCATCGCGT ATCCGATGGA CTCGGGAAC GCGCGCCGGG TCGCGGCAGA  
 3351 CGAGATGTTG ATGATCCGCC CGCCGTCGCG CAGTCGTTTC AGTCCGTGCT  
 3401 GGACCAGGAA CAGCGGTGCC CGGAC**GTTGA** CGGCGACCAG TCGGTGAG

*HincII*

3451 ACCTCCTCGG TGACTTCCGT GATCCGTCCC GAGCCGCTGA CGCCCGCGTT  
 3501 GTTCACCAGG ATGTCGAACT CGGGCGGCAC TCCGAACTCG CCCATCCCGG  
 3551 CGTCGAACGC CGCGTAGAGC CGGGCCGCGT CACCCACGAC GCGAGTTCG  
 3601 GCCCGGATGG CCAACGCCTG TCCGCCGCTG CTCCGGATGG TCTCGACGGT  
 3651 CTCTCGCGCC GCCGCCTCGC TGCTGCCGTA GTGGACTGCC ACGAGCGCCC  
 3701 CGTCCGCGGC CAGCCGCAGG GCGATAACCGC GTCCGATGCC CCGGCTTCCC  
 3751 CCGGTACCA GGGCGGTCTT GCCCTCCAGC GGTCTTCCAT ACCTCGTCCC  
 3801 ATGTGCACGC ATATCAGCCC CCGCCGTGCG TGAGCGACCC ATGGCGGCCG  
 3851 CTCGGCCGTT CGAATCGACG GTCACAGCCT ACCTGTGACC GCGTCAGACG  
 3901 GGGCCGGAGT GGCCCGGTTG GACGGCTGGG GCCAGATCGG GCGGCGCGCA  
 3951 CGGGGAACCG GCGCCGGTCA GGGGTCAAGGG GTCGCCGGGA CCGCCCAGGC  
 4001 CGGTCAAGGC ACCGACCGGA TCGAGGTCGG GCGTGCCACG CGGCCACCAAG  
 4051 TCCTCGCGGC CCAGCTCCGA CTCGTACCGC TACCAAGAGCC CGGTCCGGCC  
 4101 GAGTCTGAGC TGGACGTGGC CGCGCGGGTG GGTGAGGCAGG TTGCGGCCAGG  
 4151 GCGGGAAGGC GGGGAGGTCTG GCGGCGAGCA TCATGGGGCG GCGCGGGTCG  
 4201 AAACGGCCGG CCGCGGGTC CCAGGGCTCC TCCAGGACGT CTAGACCCGC  
 4251 CAACCCGCC CCGCGCCAGG CGCGACGGC CCGCGCCAGC TCCGCCGTGT  
 4301 CGCGTCCGGC GGCGAGGCG AGCGACGCGT AGAGCGCGCG **GGTACC**

*KpnI*